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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/774,681

DATE: 09/24/2001  
TIME: 11:27:25

Input Set : D:\31333-20001.txt  
Output Set: N:\CRF3\09242001\I774681.raw

4 <110> APPLICANT: Sunol Molecular Corporatiopn  
5 Sherman, Linda  
6 Lustgarten, Joseph  
8 <120> TITLE OF INVENTION: RECOMBINANT CONSTRUCTS ENCODING T CELL  
9 RECEPTORS SPECIFIC FOR HUMAN HLA-RESTRICTED TUMOR ANTIGENS  
12 <130> FILE REFERENCE: 31333-20001.01  
14 <140> CURRENT APPLICATION NUMBER: US 09/774,681  
15 <141> CURRENT FILING DATE: 2001-02-01  
17 <150> PRIOR APPLICATION NUMBER: US 08/812,393  
18 <151> PRIOR FILING DATE: 1997-03-05  
20 <150> PRIOR APPLICATION NUMBER: US 60/012,845  
21 <151> PRIOR FILING DATE: 1996-03-05  
23 <160> NUMBER OF SEQ ID NOS: 65  
25 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
27 <210> SEQ ID NO: 1  
28 <211> LENGTH: 1350  
29 <212> TYPE: DNA  
30 <213> ORGANISM: Artificial Sequence  
32 <220> FEATURE:  
33 <223> OTHER INFORMATION: Polynucleotide derivative of effective T cell  
34 receptor  
36 <221> NAME/KEY: CDS  
37 <222> LOCATION: (1)...(1350)  
39 <400> SEQUENCE: 1  
40 ctc gag atg cag agg aac ctg gga gct gtg ctg ggg att ctg tgg gtg 48  
41 Leu Glu Met Gln Arg Asn Leu Gly Ala Val Leu Gly Ile Leu Trp Val  
42 1 5 10 15  
44 cag att tgc tgg ctg aaa gaa cag caa gtc cag cag agt ccc gca tcc 96  
45 Gln Ile Cys Trp Leu Lys Glu Gln Gln Val Gln Gln Ser Pro Ala Ser  
46 20 25 30  
48 ttg gtt ctg cag gag ggg gag aac gca gag ctc cag tgt agc ttt tcc 144  
49 Leu Val Leu Gln Glu Gly Glu Asn Ala Glu Leu Gln Cys Ser Phe Ser  
50 35 40 45  
52 atc ttt aca aac cag gtc cag tgg ttt tac caa cgt cct ggg gga aga 192  
53 Ile Phe Thr Asn Gln Val Gln Trp Phe Tyr Gln Arg Pro Gly Gly Arg  
54 50 55 60  
56 ctc gtc agc ctg ttg tac aat cct tct ggg aca aag cag agt ggg aga 240  
57 Leu Val Ser Leu Leu Tyr Asn Pro Ser Gly Thr Lys Gln Ser Gly Arg  
58 65 70 75 80  
60 ctg aca tcc aca aca gtc att aaa gaa cgt cgc agc tct ttg cac att 288  
61 Leu Thr Ser Thr Val Ile Lys Glu Arg Arg Ser Ser Leu His Ile  
62 85 90 95  
64 tcc tcc tcc cag atc aca gac tca ggc act tat ctc tgt gcc tca aat 336  
65 Ser Ser Ser Gln Ile Thr Asp Ser Gly Thr Tyr Leu Cys Ala Ser Asn  
66 100 105 110  
68 tct gga gga agc aat gca aag cta acc ttc ggg aaa ggc act aaa ctc 384  
69 Ser Gly Gly Ser Asn Ala Lys Leu Thr Phe Gly Lys Gly Thr Lys Leu

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70	115	120	125	
72	tct gtt aaa tca ggt ggc gga ggg tct ggc ggg ggt gga tcc ggg ggt			432
73	Ser Val Lys Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly			
74	130	135	140	
76	gga ggc tca gag gct gca acc caa agc cca aga aac aag gtg gca			480
77	Gly Ser Glu Ala Ala Val Thr Gln Ser Pro Arg Asn Lys Val Ala			
78	145	150	155	160
80	gta aca gga gga aag gtg aca ttg agc tgt aat cag act aat aac cac			528
81	Val Thr Gly Gly Lys Val Thr Leu Ser Cys Asn Gln Thr Asn Asn His			
82	165	170	175	
84	aac aac atg tac tgg tat cgg cag gac acg ggg cat ggg ctg agg ctg			576
85	Asn Asn Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu			
86	180	185	190	
88	atc cat tat tca tat ggt gct ggc agc act gag aaa gga gat atc cct			624
89	Ile His Tyr Ser Tyr Gly Ala Gly Ser Thr Glu Lys Gly Asp Ile Pro			
90	195	200	205	
92	gat gga tac aag gcc tcc aga cca agc caa gag aac ttc tcc ctc att			672
93	Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile			
94	210	215	220	
96	gtg gag ttg ggt acc ccc tct cag aca tca gtg tac ttc tgt gcc agc			720
97	Val Glu Leu Gly Thr Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser			
98	225	230	235	240
100	ggt gag aca ggg acc aac gaa aga tta ttt ttc ggt cat gga acc aag			768
101	Gly Glu Thr Gly Thr Asn Glu Arg Leu Phe Phe Gly His Gly Thr Lys			
102	245	250	255	
104	ctg tct gtc ctg act agt aac tcc atc atg tac ttc agc cac ttc gtg			816
105	Leu Ser Val Leu Thr Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val			
106	260	265	270	
108	ccg gtc ttc ctg cca gcg aag ccc acc acg acg cca gcg ccg cga cca			864
109	Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Pro Ala Pro Arg Pro			
110	275	280	285	
112	cca aca ccg gcg ccc acc atc gcg tcg cag ccc ctg tcc ctg cgc cca			912
113	Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro			
114	290	295	300	
116	tct agt tct aga gat ccc aaa ctc tgc tac ctg ctg gat gga atc ctc			960
117	Ser Ser Ser Arg Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu			
118	305	310	315	320
120	ttc atc tat ggt gtc att ctc act gcc ttg ttc ctg aga gtg aag ttc			1008
121	Phe Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe			
122	325	330	335	
124	agc agg agc gca gac gcc ccc gcg tac cag cag ggc cag aac cag ctc			1056
125	Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu			
126	340	345	350	
128	tat aac gag ctc aat cta gga cga aga gag gag tac gat gtt ttg gac			1104
129	Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp			
130	355	360	365	
132	aag aga cgt ggc cgg gac cct gag atg ggg gga aag ccg aga agg aag			1152
133	Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys			
134	370	375	380	

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136 aac cct cag gaa ggc ctg tac aat gaa ctg cag aaa gat aag atg gcg	1200
137 Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala	
138 385 390 395 400	
140 gag gcc tac agt gag att ggg atg aaa ggc gag cgc cgg agg ggc aag	1248
141 Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys	
142 405 410 415	
144 ggg cac gat ggc ctt tac cag ggt ctc agt aca gcc acc aag gac acc	1296
145 Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr	
146 420 425 430	
148 tac gac gcc ctt cac atg cag gcc ctg ccc cct cgc taa gcg gcc gcc	1344
149 Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg * Ala Ala Ala	
150 435 440 445	
152 acc gcg	1350
153 Thr Ala	
157 <210> SEQ ID NO: 2	
158 <211> LENGTH: 449	
159 <212> TYPE: PRT	
160 <213> ORGANISM: Artificial Sequence	
162 <220> FEATURE:	
163 <223> OTHER INFORMATION: Deduced amino acid derivative of effective T cell receptor	
166 <400> SEQUENCE: 2	
167 Leu Glu Met Gln Arg Asn Leu Gly Ala Val Leu Gly Ile Leu Trp Val	
168 1 5 10 15	
169 Gln Ile Cys Trp Leu Lys Glu Gln Gln Val Gln Gln Ser Pro Ala Ser	
170 20 25 30	
171 Leu Val Leu Gln Glu Gly Glu Asn Ala Glu Leu Gln Cys Ser Phe Ser	
172 35 40 45	
173 Ile Phe Thr Asn Gln Val Gln Trp Phe Tyr Gln Arg Pro Gly Gly Arg	
174 50 55 60	
175 Leu Val Ser Leu Leu Tyr Asn Pro Ser Gly Thr Lys Gln Ser Gly Arg	
176 65 70 75 80	
177 Leu Thr Ser Thr Thr Val Ile Lys Glu Arg Arg Ser Ser Leu His Ile	
178 85 90 95	
179 Ser Ser Ser Gln Ile Thr Asp Ser Gly Thr Tyr Leu Cys Ala Ser Asn	
180 100 105 110	
181 Ser Gly Gly Ser Asn Ala Lys Leu Thr Phe Gly Lys Gly Thr Lys Leu	
182 115 120 125	
183 Ser Val Lys Ser Gly Gly Ser Gly Gly Gly Ser Gly Gly	
184 130 135 140	
185 Gly Gly Ser Glu Ala Ala Val Thr Gln Ser Pro Arg Asn Lys Val Ala	
186 145 150 155 160	
187 Val Thr Gly Gly Lys Val Thr Leu Ser Cys Asn Gln Thr Asn Asn His	
188 165 170 175	
189 Asn Asn Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu	
190 180 185 190	
191 Ile His Tyr Ser Tyr Gly Ala Gly Ser Thr Glu Lys Gly Asp Ile Pro	
192 195 200 205	
193 Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile	

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194	210	215	220													
195	Val	Glu	Leu	Gly	Thr	Pro	Ser	Gln	Thr	Ser	Val	Tyr	Phe	Cys	Ala	Ser
196	225															240
197	Gly	Glu	Thr	Gly	Thr	Asn	Glu	Arg	Leu	Phe	Phe	Gly	His	Gly	Thr	Lys
198																255
199	Leu	Ser	Val	Leu	Thr	Ser	Asn	Ser	Ile	Met	Tyr	Phe	Ser	His	Phe	Val
200																270
201	Pro	Val	Phe	Leu	Pro	Ala	Lys	Pro	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro
202																285
203	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro
204																300
205	Ser	Ser	Ser	Arg	Asp	Pro	Lys	Leu	Cys	Tyr	Leu	Leu	Asp	Gly	Ile	Leu
206																320
207	Phe	Ile	Tyr	Gly	Val	Ile	Leu	Thr	Ala	Leu	Phe	Leu	Arg	Val	Lys	Phe
208																335
209	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu
210																350
211	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp
212																365
213	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys
214																380
215	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala
216																400
217	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys
218																415
219	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr
220																430
221	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg	Ala	Ala	Ala	Thr
222																445
223	Ala															
226	<210>	SEQ ID NO:	3													
227	<211>	LENGTH:	24													
228	<212>	TYPE:	DNA													
229	<213>	ORGANISM:	Artificial Sequence													
231	<220>	FEATURE:														
232	<223>	OTHER INFORMATION:	Primer													
234	<400>	SEQUENCE:	3													
235	cccaaggcac	tgatgttcat	cttc													24
237	<210>	SEQ ID NO:	4													
238	<211>	LENGTH:	27													
239	<212>	TYPE:	DNA													
240	<213>	ORGANISM:	Artificial Sequence													
242	<220>	FEATURE:														
243	<223>	OTHER INFORMATION:	Primer													
245	<400>	SEQUENCE:	4													
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248	<210>	SEQ ID NO:	5													
249	<211>	LENGTH:	26													
250	<212>	TYPE:	DNA													

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Input Set : D:\31333-20001.txt  
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251 <213> ORGANISM: Primer  
253 <220> FEATURE:  
254 <223> OTHER INFORMATION: Primer  
256 <400> SEQUENCE: 5  
257 ctgcagctgc tcctcaagta ctattc 26  
259 <210> SEQ ID NO: 6  
260 <211> LENGTH: 28  
261 <212> TYPE: DNA  
262 <213> ORGANISM: Artificial Sequence  
264 <220> FEATURE:  
265 <223> OTHER INFORMATION: Primer  
267 <400> SEQUENCE: 6  
268 tcccgagaaa ggtccacagt tcctcttt 28  
270 <210> SEQ ID NO: 7  
271 <211> LENGTH: 29  
272 <212> TYPE: DNA  
273 <213> ORGANISM: Artificial Sequence  
275 <220> FEATURE:  
276 <223> OTHER INFORMATION: Primer  
278 <400> SEQUENCE: 7  
279 gaagcagcag agggttgaa gccacatac 29  
281 <210> SEQ ID NO: 8  
282 <211> LENGTH: 27  
283 <212> TYPE: DNA  
284 <213> ORGANISM: Artificial Sequence  
286 <220> FEATURE:  
287 <223> OTHER INFORMATION: Primer  
289 <400> SEQUENCE: 8  
290 ggcagggtctt cagttgctta tgaaggt 27  
292 <210> SEQ ID NO: 9  
293 <211> LENGTH: 27  
294 <212> TYPE: DNA  
295 <213> ORGANISM: Artificial Sequence  
297 <220> FEATURE:  
298 <223> OTHER INFORMATION: Primer  
300 <400> SEQUENCE: 9  
301 ggttcctt cagcgtccag aatatgt 27  
303 <210> SEQ ID NO: 10  
304 <211> LENGTH: 27  
305 <212> TYPE: DNA  
306 <213> ORGANISM: Artificial Sequence  
308 <220> FEATURE:  
309 <223> OTHER INFORMATION: Primer  
311 <400> SEQUENCE: 10  
312 gcgaaact caccctggac tgttcat 27  
314 <210> SEQ ID NO: 11  
315 <211> LENGTH: 30  
316 <212> TYPE: DNA  
317 <213> ORGANISM: Artificial Sequence

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/774,681

DATE: 09/24/2001  
TIME: 11:27:26

Input Set : D:\31333-20001.txt  
Output Set: N:\CRF3\09242001\I774681.raw